

SEQUENCE LISTING

<110> Wakamiya, N.
<120> Novel Collectin
<130> 19036/37157
<150> JP HEI 10-237611
<151> 1998-08-24
<160> 32
<210> 1
<211> 2024
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (670)..(1695)

<400> 1
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aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc 180
aagaacgact ttcaaaaatct gcagcaggtt tttcttcaag ccaagaagga cagggtattgg 240
ctgaaggaga aagtgcagag cttgcagacg ctggctgcca acaactctgc gttggccaaa 300
gccaacaacg acaccctgga ggatatgaac agccagctca actcattcac aggtcagatg 360
gagaacatca ccactatctc tcaagccaac gagcagaacc tgaaagacct gcaggactta 420
cacaaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag 480
ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg 540
cggacgctga ccagcaatct aaatgaagtc aggaccactt gcacagatac ctttaccaaa 600
cacacagatg atctgacctc cttgaataat accctggcca acatccgttt ggattctgtt 660
tctctcagg atg caa caa gat ttg atg agg tcg agg tta gac act gaa gta 711
Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val
1 5 10
gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag 759
Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys
15 20 25 30
cat ggt cag ctc atc aag aat ttt aca ata cta caa ggt cca ccg ggc 807
His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly
35 40 45
ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca 855
Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro
50 55 60
act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct 903
Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro
65 70 75
ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga 951
Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly
80 85 90
gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc 999
Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser
95 100 105 110
cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca 1047
Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro
115 120 125
ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc 1095
Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly
130 135 140

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cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg 1143
Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val
145 150 155
cct gga cct cgg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca 1191
Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro
160 165 170
ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg 1239
Gly Pro Lys Gly Pro Gly Pro Gly Pro Gly Pro Ser Gly Ala Val Val
175 180 185 190
ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc 1287
Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly
195 200 205
tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca 1335
Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser
210 215 220
gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag 1383
Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys
225 230 235
tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata 1431
Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile
240 245 250
aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac 1479
Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp
255 260 265 270
tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac 1527
Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp
275 280 285
tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat 1575
Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His
290 295 300
ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac 1623
Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn
305 310 315
gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg 1671
Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg
320 325 330
gag aca gta ctg tca tct gca tta taacggactg tgatgggac acatgagcaa 1725
Glu Thr Val Leu Ser Ser Ala Leu
335 340
atttttcagct ctcaaaggca aaggacactc cttttctaatt gcatcacctt ctcacatcagat 1785
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taccatccgt cattacccaa agacttgga actaaaatgt tccccagggt gatagtctga 1905
ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965
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<210> 2

<211> 547

<212> PRT

<213> Homo Sapiens

<220>

<223> Deduced Amino Acid Sequence of Novel Collectin from Nucleotide Sequence

<400>2

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Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu
1 5 10 15
Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val
20 25 30
Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn
35 40 45
Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys
50 55 60

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[illegible]

<210> 3
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified Consensus Sequence of collectins Hybridizable with Novel Collectin

<400>3
 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn
 1 5 10 15
 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe
 20 25

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Reverse Primer for Screening a Novel Collectin.

<400> 4
 caatctgatg agaagtgat g 21

<210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Forward Primer for Screening a Novel Collectin.

<400> 5
 acgaggggct ggatgggaca t 21

<210> 6
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence of three collectins which were reported heretofore

<400>6
 Glu Asp Cys Val Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro
 1 5 10 15
 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe
 20 25

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> M13 Universal Primer Sequence for Sequencing

<400> 7
 cgacgttgta aaacgacggc cagt 24

<210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> M13 Reverse Primer Sequence for Sequencing.

<400> 8
 caggaaaca gctatgac 17

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a lambda gt11 Reverse Primer for Sequencing.

<400> 9
 ttgacaccag accaactggt aatg 24

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a lambda gt11 Forward Primer for Sequencing.

<400> 10
 ggtggcgacg actcctggag cccg 24

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Screening a Novel Collectin

<400>11
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<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Screening a Novel Collectin

<400>12
 ttttatccat tgctgttcct c 21

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Sequencing a Novel Collectin

<400>13
 ctggcagtc cccgaggtcca g 21

 <210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Primer for Sequencing a Novel Collectin

 <400>14
 gctggtcccc ccgagagcg t 21

 <210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a 1RC2 Primer for Cap Site Sequencing

 <400> 15
 caaggtacgc cacagcgat g 21

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Synthetic TGP1 Primer for Cap Site Sequencing

 <400> 16
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 <210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a 2RC2 Primer for Cap Site Sequencing

 <400> 17
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 <210> 18
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Synthetic TGP2 Primer for Cap Site Sequencing

 <400> 18
 cattcttgac aaacttcata g 21

 <210> 19
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Screening a Novel Collectin

 <400> 19
 gaagacaagt cttcaactct tg 22

 <210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Primer for Screening a Novel Collectin

 <400> 20
 ctctgagtct gtgaggccga tc 22

 <210> 21
 <211> 111
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Probe for Screening a Novel Collectin

 <400> 21
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 aaacagatgg tagggagaga gagccactgg atcggcctca cagactcaga g 111

 <210> 22
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Forward Primer for Screening a Novel Collectin

 <400> 22
 gtgcccctgg ccctgcagaa tg 22

 <210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Reverse Primer for Screening a Novel Collectin

 <400> 23
 gcatatcacc ctggggaaca ttttag 26

 <210> 24
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Sense Primer for Screening Beta Actin

 <400> 24
 caagagatgg ccacggctgc t 21

 <210> 25

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of an Antisense Primer for Screening Beta Actin

<400> 25
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<210> 26
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Sense Primer for Amplifying the Novel Collectin.

<400> 26
 aaggaaaaaa gcggccgcat gcaacaagat ttgatgagg 39

<210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Reverse Primer for Amplifying the Novel Collectin

<400> 27
 gctctagatt ataatgcaga tgacagtac 29

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 28
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<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 29
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<210> 30
 <211> 248
 <212> PRT
 <213> Homo sapiens

<220>
 <223> mannan-binding protein (MBP)

<400> 30

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
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 20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
 35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
 50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
 65 70 75 80

~~Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp~~
 85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
 100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
 115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
 130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
 145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
 165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
 180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
 195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
 210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
 225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
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<210> 31

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<223> surfactant protein A (SP-A)

<400> 31

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Gly Ala Ala Cys Glu Val Lys Asp Val Cys Val Gly Ser Pro Gly Ile
 20 25 30
 Pro Gly Thr Pro Gly Ser His Gly Leu Pro Gly Arg Asp Gly Arg Asp
 35 40 45
 Gly Val Lys Gly Asp Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly
 50 55 60
 Glu Thr Pro Cys Pro Pro Gly Asn Asn Gly Leu Pro Gly Ala Pro Gly
 65 70 75 80
 Val Pro Gly Glu Arg Gly Glu Lys Gly Glu Pro Gly Glu Arg Gly Pro
 85 90 95
 Pro Gly Leu Pro Ala His Leu Asp Glu Glu Leu Gln Ala Thr Leu His
 100 105 110
 Asp Phe Arg His Gln Ile Leu Gln Thr Arg Gly Ala Leu Ser Leu Gln
 115 120 125
 Gly Ser Ile Met Thr Val Gly Glu Lys Val Phe Ser Ser Asn Gly Gln
 130 135 140
 Ser Ile Thr Phe Asp Ala Ile Gln Glu Ala Cys Ala Arg Ala Gly Gly
 145 150 155 160
 Arg Ile Ala Val Pro Arg Asn Pro Glu Glu Asn Glu Ala Ile Ala Ser
 165 170 175
 Phe Val Lys Lys Tyr Asn Thr Tyr Ala Tyr Val Gly Leu Thr Glu Gly
 180 185 190
 Pro Ser Pro Gly Asp Phe Arg Tyr Ser Asp Gly Thr Pro Val Asn Tyr
 195 200 205
 Thr Asn Trp Tyr Arg Gly Glu Pro Ala Gly Arg Gly Lys Glu Gln Cys
 210 215 220
 Val Glu Met Tyr Thr Asp Gly Gln Trp Asn Asp Arg Asn Cys Leu Tyr
 225 230 235 240
 Ser Arg Leu Thr Ile Cys Glu Phe
 245

<210> 32

<211> 375

<212> PRT

<213> Homo sapiens

<220>

<223> surfactant protein D (SP-D)

<400> 32

Met Leu Leu Phe Leu Leu Ser Ala Leu Val Leu Leu Thr Gln Pro Leu
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Gly Tyr Leu Glu Ala Glu Met Lys Thr Tyr Ser His Arg Thr Thr Pro
 20 25 30

Ser Ala Cys Thr Leu Val Met Cys Ser Ser Val Glu Ser Gly Leu Pro
 35 40 45

